RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/538,000
Source: IFW0
Date Processed by STIC: 11/7/2006

ENTERED

IFWO

RAW SEQUENCE LISTING DATE: 11/07/2006
PATENT APPLICATION: **US/10/538,000** TIME: 11:46:38

Input Set : **N:\Crf4\11032006\K538000.raw**
Output Set: **N:\CRF4\11072006\J538000.raw**

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      1 <110> APPLICANT: DSM IP Assets B.V.
      2       Pieter J.A.M. PLOMP
      3       Lex DE BOER
      4       Rutger J. VAN ROOIJEN
      5       Roelf B. MEIMA
      6 <120> TITLE OF INVENTION: NOVEL FOOD PRODUCTION PROCESS
      7 <130> FILE REFERENCE: 4662-25 / 21401USWO
C-->  8 <140> CURRENT APPLICATION NUMBER: US/10/538,000
      9 <141> CURRENT FILING DATE: 2005-06-09
     10 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014553
     11 <151> PRIOR FILING DATE: 2003-12-18
     12 <150> PRIOR APPLICATION NUMBER: EP 02102819.6
     13 <151> PRIOR FILING DATE: 2002-12-19
     14 <160> NUMBER OF SEQ ID NOS: 3
     15 <170> SOFTWARE: MS Word
     17 <210> SEQ ID NO: 1
     18 <211> LENGTH: 3223
     19 <212> TYPE: DNA
     20 <213> ORGANISM: Aspergillus niger
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     24       ggctccgaga gttttgatag cagtagccaa ttaactagta gatgctagta ctactctagt     180
     25       aatttggggg cgaatgttga atccagctca tgccaattga catctggaga tctccacgag     240
     26       acaacgagat aagatgaaat attgctgtca tgggtgataa ctagatgctt cgagaaggat     300
     27       tcttgaggat tgcctcatcg catgggataa tatcaccctc gggtggacct tcccggctgt     360
     28       tggggcttat cgtggaagag tcacccccga tatcggtggg ccaagccctt tatcaatcat     420
     29       catcctatca gtttccaccc acaagatagc ctatggaccc tgattccctt ctagccacag     480
     30       agactagtac tagtctatca tgtcgactcc atgtggagaa accctgataa gaccatgtgg     540
     31       aggaggagat agcaagcctc cacagaaaca atatcatctc cacctgcaat cacggttgga     600
     32       ttccgaatac acccgccgcc tggcaagcac atggggtata aaatgctgaa accaggcaag     660
     33       atgaattgga agagaagcca gcagagacca tcgcatccgt cttcatcatg cctctcaagc     720
     34       cgattctcct gtctgccctg gccagtctcg cctcggcctc tccgctgctc tactcgcgga     780
     35       ccaccaatga aaccttcgtc ttcaccaatg ccaatggcct caacttcacc cagatgaaca     840
     36       ccaccctgcc gaacgtgacc attttcgcaa cgggtaggtg gaccgagtat acctcaggta     900
     37       gtgcgaccga tagttaaccg caactcacag gtggtaccat cgcgggctcc gattccagct     960
     38       caaccgccac gaccggctac acctccggag cagtcggggt cctgtccctc atcgatgcgg    1020
     39       tgccatccat gctggatgtg gccaatgttg ccggcgtcca ggtggccaac gtgggaagcg    1080
     40       aggatatcac ctctgacatc ctgatttcca tgtccaagaa gctgaaccgc gttgtatgtg    1140
     41       aggacccgac catggccggt gctgtcatca cccacggcac cgacaccctc gaggagactg    1200
     42       ccttcttcct ggacgccact gtcaactgtg gcaagccaat tgtcatcgtg ggtgccatgc    1260
     43       gcccatccac ggccatctca gctgacgggc ccttcaatct gctcgaagcc gtgacggtgg    1320
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45       cggcctacta tgtgaccaag accaatgcca acactatgga caccttcaag gccatggaga     1440
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47       caaccggtaa ggtggccttt gacatcacca acgtgactga gatcccccgt gtggacattc     1560
48       tgttttctta tgaggacatg cacaacgaca ccctctacaa cgccatctcc agtggtgccc     1620
49       agggaattgt ggtgagtgtg atttccttga tctctctcta taaaacttgg aatggacgct     1680
50       gatgagaata gattgccggg gctggtgctg gaggcgtcac aacctccttc aatgaggcta     1740
51       tcgaggatgt catcaaccgt ttggagatcc ctgtcgtgca gagtatgcgc acagtcaatg     1800
52       gggaagtgcc actgtcagac gtgagcagcg acaccgccac ccacatcgcc agtggatacc     1860
53       taaacccgca gaagtcccgc attctgttgg gattgctgct atcccaggga aagaatatca     1920
54       ccgaaatcgc tgacgtgttt gctctgggca cggatgcgta ggtgtcgata gaaccattgt     1980
55       atataataat gaccggatat tatgatcatg atagattgca atagaaagtg actggataca     2040
56       catcagcaaa ggataccgag ttttgccctc aggcgttcgt agaaaaagtg tatcctactg     2100
57       aagatcatga atcatgtctt atcttctggc cccctcgtat ccagggtgtt ggacatgcag     2160
58       ggtgctttgc gtctgaagga tccgagatca aattgacacg agccagagtc tgatacatcc     2220
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60       agctagggcc tggcttggtg gcatatcgtt ggactaatag atggtagttc aattaccgac     2340
61       gggactgtct cccgccatta ttctcacaat tcttatcagc acattttccc tgtcgcgctt     2400
62       ggatctgcaa tatttatttc cctcgtcatc acattcccac gaaaagacca tccagacatc     2460
63       ttgctcggta ttctggaccg taagactgtt ttgaaaggca aatgtaaagc gtgattggtc     2520
64       gacgtcaagc ctgaccaatc tagtaagctg gtcttacttt gggtgtagac ggaggtatta     2580
65       ggtagtatta aggcagctag ttcgcctgca ttaccaccca ggcgaggcac gccactgctg     2640
66       atcaggcgcg aaatggaacg aagtgcgagg tccacttaac atgatgcgcg cggatactaa     2700
67       ggcgaccaag accctggatt gatcgctatg attcgcggaa ccccgcgggt tcttcacggc     2760
68       tttcgataac gcaggattgg atcctcccag cctcgtctct gcaagtggga ccctgaaggg     2820
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71       tcctagcctg ctggtagagg cggatgatta taataatcaa agcaccctat cgtaaggatg     3000
72       aaggcttgtc cctggtcaac catcactctg gttattgact agttgtgttt gggagacagc     3060
73       tgaagcccat tgtcggtaat cgtccccaaa gaatctgccc ctgcatcatg gagtcaggaa     3120
74       agaccgggtt tcgcacggtc gcagaaccgc atccaacacg tctagtagaa ggaggggtag     3180
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77 <210> SEQ ID NO: 2
78 <211> LENGTH: 1137
79 <212> TYPE: DNA
80 <213> ORGANISM: Aspergillus niger
81 <220> FEATURE:
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83 <222> LOCATION: (1)..(1137)
84 <400> SEQUENCE: 2
85       atg cct ctc aag ccg att ctc ctg tct gcc ctg gcc agt ctc gcc tcg       48
86       Met Pro Leu Lys Pro Ile Leu Leu Ser Ala Leu Ala Ser Leu Ala Ser
87       1               5                  10                  15
88       gcc tct ccg ctg ctc tac tcg cgg acc acc aat gaa acc ttc gtc ttc       96
89       Ala Ser Pro Leu Leu Tyr Ser Arg Thr Thr Asn Glu Thr Phe Val Phe
90                   20                  25                  30
91       acc aat gcc aat ggc ctc aac ttc acc cag atg aac acc acc ctg ccg      144
92       Thr Asn Ala Asn Gly Leu Asn Phe Thr Gln Met Asn Thr Thr Leu Pro
93               35                  40                  45
94       aac gtg acc att ttc gca acg ggt ggt acc atc gcg ggc tcc gat tcc      192
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98       Ser Ser Thr Ala Thr Thr Gly Tyr Thr Ser Gly Ala Val Gly Val Leu
99       65                  70                  75                  80
100       tcc ctc atc gat gcg gtg cca tcc atg ctg gat gtg gcc aat gtt gcc      288
101       Ser Leu Ile Asp Ala Val Pro Ser Met Leu Asp Val Ala Asn Val Ala
102                      85                  90                  95
103       ggc gtc cag gtg gcc aac gtg gga agc gag gat atc acc tct gac atc      336
104       Gly Val Gln Val Ala Asn Val Gly Ser Glu Asp Ile Thr Ser Asp Ile
105                  100                 105                 110
106       ctg att tcc atg tcc aag aag ctg aac cgc gtt gta tgt gag gac ccg      384
107       Leu Ile Ser Met Ser Lys Lys Leu Asn Arg Val Val Cys Glu Asp Pro
108              115                 120                 125
109       acc atg gcc ggt gct gtc atc acc cac ggc acc gac acc ctc gag gag      432
110       Thr Met Ala Gly Ala Val Ile Thr His Gly Thr Asp Thr Leu Glu Glu
111          130                 135                 140
112       act gcc ttc ttc ctg gac gcc act gtc aac tgt ggc aag cca att gtc      480
113       Thr Ala Phe Phe Leu Asp Ala Thr Val Asn Cys Gly Lys Pro Ile Val
114       145                 150                 155                 160
115       atc gtg ggt gcc atg cgc cca tcc acg gcc atc tca gct gac ggg ccc      528
116       Ile Val Gly Ala Met Arg Pro Ser Thr Ala Ile Ser Ala Asp Gly Pro
117                      165                 170                 175
118       ttc aat ctg ctc gaa gcc gtg acg gtg gct gcc tcc acg tcg gcg cgc      576
119       Phe Asn Leu Leu Glu Ala Val Thr Val Ala Ala Ser Thr Ser Ala Arg
120                  180                 185                 190
121       gat cgc ggt gcc atg gtg gtc atg aac gat cgc att gcc tcg gcc tac      624
122       Asp Arg Gly Ala Met Val Val Met Asn Asp Arg Ile Ala Ser Ala Tyr
123              195                 200                 205
124       tat gtg acc aag acc aat gcc aac act atg gac acc ttc aag gcc atg      672
125       Tyr Val Thr Lys Thr Asn Ala Asn Thr Met Asp Thr Phe Lys Ala Met
126          210                 215                 220
127       gag atg ggc tac ctt ggc gag atg atc tcc aac acc cct ttc ttc ttc      720
128       Glu Met Gly Tyr Leu Gly Glu Met Ile Ser Asn Thr Pro Phe Phe Phe
129       225                 230                 235                 240
130       tac ccg ccc gtc aag cca acc ggt aag gtg gcc ttt gac atc acc aac      768
131       Tyr Pro Pro Val Lys Pro Thr Gly Lys Val Ala Phe Asp Ile Thr Asn
132                      245                 250                 255
133       gtg act gag atc ccc cgt gtg gac att ctg ttt tct tat gag gac atg      816
134       Val Thr Glu Ile Pro Arg Val Asp Ile Leu Phe Ser Tyr Glu Asp Met
135                  260                 265                 270
136       cac aac gac acc ctc tac aac gcc atc tcc agt ggt gcc cag gga att      864
137       His Asn Asp Thr Leu Tyr Asn Ala Ile Ser Ser Gly Ala Gln Gly Ile
138              275                 280                 285
139       gtg att gcc ggg gct ggt gct gga ggc gtc aca acc tcc ttc aat gag      912
140       Val Ile Ala Gly Ala Gly Ala Gly Gly Val Thr Thr Ser Phe Asn Glu
141          290                 295                 300
142       gct atc gag gat gtc atc aac cgt ttg gag atc cct gtc gtg cag agt      960
143       Ala Ile Glu Asp Val Ile Asn Arg Leu Glu Ile Pro Val Val Gln Ser
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144       305                 310                 315                 320
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146       Met Arg Thr Val Asn Gly Glu Val Pro Leu Ser Asp Val Ser Ser Asp
147                       325                 330                 335
148       acc gcc acc cac atc gcc agt gga tac cta aac ccg cag aag tcc cgc       1056
149       Thr Ala Thr His Ile Ala Ser Gly Tyr Leu Asn Pro Gln Lys Ser Arg
150                 340                 345                 350
151       att ctg ttg gga ttg ctg cta tcc cag gga aag aat atc acc gaa atc       1104
152       Ile Leu Leu Gly Leu Leu Leu Ser Gln Gly Lys Asn Ile Thr Glu Ile
153               355                 360                 365
154       gct gac gtg ttt gct ctg ggc acg gat gcg tag                           1137
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156           370                 375
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159 <211> LENGTH: 378
160 <212> TYPE: PRT
161 <213> ORGANISM: Aspergillus niger
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165       Ala Ser Pro Leu Leu Tyr Ser Arg Thr Thr Asn Glu Thr Phe Val Phe
166                   20                  25                  30
167       Thr Asn Ala Asn Gly Leu Asn Phe Thr Gln Met Asn Thr Thr Leu Pro
168               35                  40                  45
169       Asn Val Thr Ile Phe Ala Thr Gly Gly Thr Ile Ala Gly Ser Asp Ser
170           50                  55                  60
171       Ser Ser Thr Ala Thr Thr Gly Tyr Thr Ser Gly Ala Val Gly Val Leu
172       65                  70                  75                  80
173       Ser Leu Ile Asp Ala Val Pro Ser Met Leu Asp Val Ala Asn Val Ala
174                       85                  90                  95
175       Gly Val Gln Val Ala Asn Val Gly Ser Glu Asp Ile Thr Ser Asp Ile
176                   100                 105                 110
177       Leu Ile Ser Met Ser Lys Lys Leu Asn Arg Val Val Cys Glu Asp Pro
178               115                 120                 125
179       Thr Met Ala Gly Ala Val Ile Thr His Gly Thr Asp Thr Leu Glu Glu
180           130                 135                 140
181       Thr Ala Phe Phe Leu Asp Ala Thr Val Asn Cys Gly Lys Pro Ile Val
182       145                 150                 155                 160
183       Ile Val Gly Ala Met Arg Pro Ser Thr Ala Ile Ser Ala Asp Gly Pro
184                       165                 170                 175
185       Phe Asn Leu Leu Glu Ala Val Thr Val Ala Ala Ser Thr Ser Ala Arg
186                   180                 185                 190
187       Asp Arg Gly Ala Met Val Val Met Asn Asp Arg Ile Ala Ser Ala Tyr
188               195                 200                 205
189       Tyr Val Thr Lys Thr Asn Ala Asn Thr Met Asp Thr Phe Lys Ala Met
190           210                 215                 220
191       Glu Met Gly Tyr Leu Gly Glu Met Ile Ser Asn Thr Pro Phe Phe Phe
192       225                 230                 235                 240
193       Tyr Pro Pro Val Lys Pro Thr Gly Lys Val Ala Phe Asp Ile Thr Asn
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                    245                 250                 255
Val Thr Glu Ile Pro Arg Val Asp Ile Leu Phe Ser Tyr Glu Asp Met
            260                 265                 270
His Asn Asp Thr Leu Tyr Asn Ala Ile Ser Ser Gly Ala Gln Gly Ile
        275                 280                 285
Val Ile Ala Gly Ala Gly Ala Gly Gly Val Thr Thr Ser Phe Asn Glu
    290                 295                 300
Ala Ile Glu Asp Val Ile Asn Arg Leu Glu Ile Pro Val Val Gln Ser
305                 310                 315                 320
Met Arg Thr Val Asn Gly Glu Val Pro Leu Ser Asp Val Ser Ser Asp
                    325                 330                 335
Thr Ala Thr His Ile Ala Ser Gly Tyr Leu Asn Pro Gln Lys Ser Arg
            340                 345                 350
Ile Leu Leu Gly Leu Leu Leu Ser Gln Gly Lys Asn Ile Thr Glu Ile
        355                 360                 365
Ala Asp Val Phe Ala Leu Gly Thr Asp Ala
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/07/2006
PATENT APPLICATION: **US/10/538,000** TIME: 11:46:39

Input Set : **N:\Crf4\11032006\K538000.raw**
Output Set: **N:\CRF4\11072006\J538000.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57
Seq#:1; Line(s) 58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75
Seq#:2; Line(s) 145,148,151,154

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/538,000**

DATE: 11/07/2006
TIME: 11:46:39

Input Set : **N:\Crf4\11032006\K538000.raw**
Output Set: **N:\CRF4\11072006\J538000.raw**

L:8 M:270 C: Current Application Number differs, Replaced Current Application Number